

Application No.: 09/482416

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/462,416

DATE: 07/30/2001

TIME: 14:57:53

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\07302001\I462416.raw

ENTERED

3 <110> APPLICANT: REVEL, Michel
4 CHEBATH, Judith
5 LAPIDOT, Tsvee
6 KOLLET, Orit
8 <120> TITLE OF INVENTION: CHIMERIC INTERLEUKIN-6 SOLUBLE RECEPTOR/LIGAND PROTEIN,
ANALOGS THEREOF
9 AND USES THEREOF
11 <130> FILE REFERENCE: REVEL=15
13 <140> CURRENT APPLICATION NUMBER: 09/462,416
14 <141> CURRENT FILING DATE: 2000-04-13
16 <150> PRIOR APPLICATION NUMBER: PCT/IL98/00321
17 <151> PRIOR FILING DATE: 1998-07-09
19 <150> PRIOR APPLICATION NUMBER: IL 121284
20 <151> PRIOR FILING DATE: 1997-07-10
22 <150> PRIOR APPLICATION NUMBER: IL 122818
23 <151> PRIOR FILING DATE: 1997-12-30
25 <160> NUMBER OF SEQ ID NOS: 12
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70 <213> ORGANISM: Artificial Sequence
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120 20 25 30
123 Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
124 35 40 45
127 Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
128 50 55 60
131 Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
132 65 70 75 80
135 Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
136 85 90 95
139 Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
140 100 105 110
143 Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
144 115 120 125
147 Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
148 130 135 140
151 Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
152 145 150 155 160
155 Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
156 165 170 175

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163 Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
164      195      200      205
167 Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
168      210      215      220
171 Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
172 225      230      235      240
175 Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
176      245      250      255
179 Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
180      260      265      270
183 Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
184      275      280      285
187 Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
188      290      295      300
191 Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
192 305      310      315      320
195 Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr
196      325      330      335
199 Asn Lys Asp Asp Asp Asn Ile Leu Phe Arg Asp Ser Ala Asn Ala Thr
200      340      345      350
203 Ser Leu Pro Val Glu Phe Met Pro Val Pro Pro Gly Glu Asp Ser Lys
204      355      360      365
207 Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile
208      370      375      380
211 Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys
212 385      390      395      400
215 Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu
216      405      410      415
219 Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys
220      420      425      430
223 Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr
224      435      440      445
227 Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe
228      450      455      460
231 Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val
232 465      470      475      480
235 Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr
236      485      490      495
239 Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala
240      500      505      510
243 Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser
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252 <211> LENGTH: 471
253 <212> TYPE: PRT

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254 <213> ORGANISM: Artificial Sequence

256 <220> FEATURE:

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269 Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr
270          35          40          45
273 Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile
274          50          55          60
277 Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser
278 65          70          75          80
281 Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala
282          85          90          95
285 Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu
286          100         105         110
289 Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr
290          115         120         125
293 Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln
294          130         135         140
297 Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn
298 145          150         155         160
301 Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu
302          165         170         175
305 Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His
306          180         185         190
309 Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala
310          195         200         205
313 Leu Arg Gln Met Gly Gly Gly Gly Asp Pro Gly Gly Gly Gly Gly Gly
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317 Pro Gly Val Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser
318 225          230         235         240
321 Pro Leu Ser Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser
322          245         250         255
325 Leu Thr Thr Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro
326          260         265         270
329 Ala Glu Asp Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys
330          275         280         285
333 Phe Ser Cys Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile
334          290         295         300
337 Val Ser Met Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr
338 305          310         315         320
341 Gln Thr Phe Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn
342          325         330         335
345 Ile Thr Val Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr
346          340         345         350
349 Trp Gln Asp Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe

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350	355	360	365	
353	Glu Leu Arg Tyr Arg Ala	Glu Arg Ser Lys Thr Phe	Thr Thr Trp Met	
354	370	375	380	
357	Val Lys Asp Leu Gln His His	Cys Val Ile His Asp Ala	Trp Ser Gly	
358	385	390	395	400
361	Leu Arg His Val Val Gln Leu Arg	Ala Gln Glu Glu Phe Gly	Gln Gly	
362	405	410	415	
365	Glu Trp Ser Glu Trp Ser Pro Glu	Ala Met Gly Thr Pro Trp Thr Glu		
366	420	425	430	
369	Ser Arg Ser Pro Pro Ala Glu Asn	Glu Val Ser Thr Pro Met Gln Ala		
370	435	440	445	
373	Leu Thr Thr Asn Lys Asp Asp	Asn Ile Leu Phe Arg Asp Ser Ala		
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VERIFICATION SUMMARY

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